

# SEQUENCE LISTING

<110> Mahajan, Pramod B.  
Tagliani, Laura

<120> Rad23 Genes and Uses Thereof

<130> 0964D

<150> 09/413,574

<151> 1999-10-06

<150> 60/109,728

<151> 1998-11-23

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<170> FastSEQ for Windows Version 3.0

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<211> 1522

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (58)...(1272)

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Lys Leu Asn Val Lys Thr Leu Lys Gly Thr Asn Phe Glu Ile Glu Ala  
5 10 15

agc ccc gat gca tcg gtt gct gat gtg aag agg atc att gag acc act 156  
Ser Pro Asp Ala Ser Val Ala Asp Val Lys Arg Ile Ile Glu Thr Thr  
20 25 30

caa ggt cag agt acc tac cgg gcg gac cag caa atg ctc ata tac caa 204  
Gln Gly Gln Ser Thr Tyr Arg Ala Asp Gln Gln Met Leu Ile Tyr Gln  
35 40 45

ggg aaa att ctc aag gat gaa acc act ttg gaa agc aac gga gtt gct 252  
Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu Ser Asn Gly Val Ala  
50 55 60 65

gag aac agc ttc ctt gtt ata atg ttg tcc aag gct aag gca tca tcg 300  
Glu Asn Ser Phe Leu Val Ile Met Leu Ser Lys Ala Lys Ala Ser Ser  
70 75 80

agt gga gct tct acc gct act act gca aaa gct cct gca act ctg gcc 348  
Ser Gly Ala Ser Thr Ala Thr Thr Ala Lys Ala Pro Ala Thr Leu Ala  
85 90 95

caa cct gct gcc cct gtg gcc cct gct gca tca gtt gca aga aca cca 396  
Gln Pro Ala Ala Pro Val Ala Pro Ala Ala Ser Val Ala Arg Thr Pro

100	105	110	
aca cag gct cct gtt gcc	aca gct gaa acg gca cct	cca agt gtc caa	444
Thr Gln Ala Pro Val Ala	Thr Ala Glu Thr Ala Pro	Pro Ser Val Gln	
115	120	125	
cct cag gct gct cca gct	gct acg gtt gct gct	act gat gat gct gat	492
Pro Gln Ala Ala Pro Gln	Ala Thr Val Ala Thr	Asp Asp Ala Asp	
130	135	140	145
gtg tac agt cag gca gct	tca aac ctt gta ttt	ggc aac aat cta gaa	540
Val Tyr Ser Gln Ala Ala	Ser Asn Leu Val Phe	Gly Asn Asn Leu Glu	
150	155	160	
cag act atc caa caa att	ctt gac atg ggt ggt	ggc aca tgg gaa cgt	588
Gln Thr Ile Gln Gln Ile	Leu Asp Met Gly Gly	Gly Thr Trp Glu Arg	
165	170	175	
gat act gtt gtt cgt gct	cta cgt gct gca tac	aat aac ccc gag aga	636
Asp Thr Val Val Arg Ala	Leu Arg Ala Ala Tyr	Asn Asn Pro Glu Arg	
180	185	190	
gct ata gac tac ctg tat	tct gga att cct gag	aat gtg gag gct cag	684
Ala Ile Asp Tyr Leu Tyr	Ser Gly Ile Pro Glu	Asn Val Glu Ala Gln	
195	200	205	
cct gtt gcc cga gca cct	gct gct ggc caa caa	aca aat cag cag gcc	732
Pro Val Ala Arg Ala Pro	Ala Ala Gly Gln Thr	Asn Gln Gln Ala	
210	215	220	225
gca tca ccc gct cag cca	gca gtt gca ttg cca	gtg cag cca tca cct	780
Ala Ser Pro Ala Gln Pro	Ala Val Ala Leu Pro	Val Gln Pro Ser Pro	
230	235	240	
gcc tct gca ggg cct aat	gca aat cct ttg aac	ctt ttt cct cag ggt	828
Ala Ser Ala Gly Pro Asn	Ala Asn Pro Leu Asn	Leu Phe Pro Gln Gly	
245	250	255	
gtt cca agt ggt ggg tcc	aac cca ggt gtt gtt	cca ggt gca gga tct	876
Val Pro Ser Gly Gly Ser	Asn Pro Gly Val Val	Pro Gly Ala Gly Ser	
260	265	270	
ggt gct ctt gat gcc ttg	cga cag ctt cca cag	ttt caa gca ctc ctt	924
Gly Ala Leu Asp Ala Leu	Arg Gln Leu Pro Gln	Phe Gln Ala Leu Leu	
275	280	285	
cag tta gtc cag gct aat	cct caa atc ttg cag	cca atg ctt caa gag	972
Gln Leu Val Gln Ala Asn	Pro Gln Ile Leu Gln	Pro Met Leu Gln Glu	
290	295	300	305
cta ggt aaa caa aac cca	caa att ctg cgg ttg	att cag gaa aat caa	1020
Leu Gly Lys Gln Asn Pro	Gln Ile Leu Arg Leu	Ile Gln Glu Asn Gln	
310	315	320	
gct gag ttt ctc cgc ttg	gtg aat gaa tct cct	gag ggt ggt cct gga	1068
Ala Glu Phe Leu Arg Leu	Val Asn Glu Ser Pro	Glu Gly Gly Pro Gly	
325	330	335	
ggg aac ata cta ggt caa	ctg gca gct gct gtg	cca caa acg ctg aca	1116
Gly Asn Ile Leu Gly Gln	Leu Ala Ala Val Pro	Gln Thr Leu Thr	
340	345	350	

gtt acc cca gag gaa cgg gag gct atc cag cgg ctc gag gga atg ggg 1164  
 Val Thr Pro Glu Glu Arg Glu Ala Ile Gln Arg Leu Glu Gly Met Gly  
 355 360 365

ttc aac cgt gag ctt gtg cta gaa gtt ttc ttt gca tgc aac aag gac 1212  
 Phe Asn Arg Glu Leu Val Leu Glu Val Phe Phe Ala Cys Asn Lys Asp  
 370 375 380 385

gaa gag ctt aca gcc aac tac ctc ctg gat cat ggc cat gag ttt gac 1260  
 Glu Glu Leu Thr Ala Asn Tyr Leu Leu Asp His Gly His Glu Phe Asp  
 390 395 400

gat cag cag caa tagacgtggg gtggatggag gaaaccgagg cagttgcaga 1312  
 Asp Gln Gln Gln  
 405

acagcgcagtg tcgtttcttat gccctctgcc tgaacgagaga tactcggctgc tctatgctat 1372  
 gctgctgact atcttttatt tccatatata ttgttcgga atgctttcta agtacctatt 1432  
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 <212> PRT  
 <213> Zea mays

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 Thr Gln Gly Gln Ser Thr Tyr Arg Ala Asp Gln Gln Met Leu Ile Tyr  
 35 40 45  
 Gln Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu Ser Asn Gly Val  
 50 55 60  
 Ala Glu Asn Ser Phe Leu Val Ile Met Leu Ser Lys Ala Lys Ala Ser  
 65 70 75 80  
 Ser Ser Gly Ala Ser Thr Ala Thr Thr Ala Lys Ala Pro Ala Thr Leu  
 85 90 95  
 Ala Gln Pro Ala Ala Pro Val Ala Pro Ala Ala Ser Val Ala Arg Thr  
 100 105 110  
 Pro Thr Gln Ala Pro Val Ala Thr Ala Glu Thr Ala Pro Pro Ser Val  
 115 120 125  
 Gln Pro Gln Ala Ala Pro Ala Ala Thr Val Ala Ala Thr Asp Asp Ala  
 130 135 140  
 Asp Val Tyr Ser Gln Ala Ala Ser Asn Leu Val Phe Gly Asn Asn Leu  
 145 150 155 160  
 Glu Gln Thr Ile Gln Gln Ile Leu Asp Met Gly Gly Thr Trp Glu  
 165 170 175  
 Arg Asp Thr Val Val Arg Ala Leu Arg Ala Ala Tyr Asn Asn Pro Glu  
 180 185 190  
 Arg Ala Ile Asp Tyr Leu Tyr Ser Gly Ile Pro Glu Asn Val Glu Ala  
 195 200 205  
 Gln Pro Val Ala Arg Ala Pro Ala Ala Gly Gln Gln Thr Asn Gln Gln  
 210 215 220  
 Ala Ala Ser Pro Ala Gln Pro Ala Val Ala Leu Pro Val Gln Pro Ser  
 225 230 235 240  
 Pro Ala Ser Ala Gly Pro Asn Ala Asn Pro Leu Asn Leu Phe Pro Gln  
 245 250 255

Gly Val Pro Ser Gly Gly Ser Asn Pro Gly Val Val Pro Gly Ala Gly  
260 265 270

Ser Gly Ala Leu Asp Ala Leu Arg Gln Leu Pro Gln Phe Gln Ala Leu  
275 280 285  
Leu Gln Leu Val Gln Ala Asn Pro Gln Ile Leu Gln Pro Met Leu Gln  
290 295 300  
Glu Leu Gly Lys Gln Asn Pro Gln Ile Leu Arg Leu Ile Gln Glu Asn  
305 310 315 320  
Gln Ala Glu Phe Leu Arg Leu Val Asn Glu Ser Pro Glu Gly Gly Pro  
325 330 335  
Gly Gly Asn Ile Leu Gly Gln Leu Ala Ala Val Pro Gln Thr Leu  
340 345 350  
Thr Val Thr Pro Glu Glu Arg Glu Ala Ile Gln Arg Leu Glu Gly Met  
355 360 365  
Gly Phe Asn Arg Glu Leu Val Leu Glu Val Phe Phe Ala Cys Asn Lys  
370 375 380  
Asp Glu Glu Leu Thr Ala Asn Tyr Leu Leu Asp His Gly His Glu Phe  
385 390 395 400  
Asp Asp Gln Gln Gln  
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Met Lys Leu Thr  
1  
  
gtg aag acc ctc aag gga acg cac ttc gag atc cgg gtg cag ccc aac 165  
Val Lys Thr Leu Lys Gly Thr His Phe Glu Ile Arg Val Gln Pro Asn  
5 10 15 20  
  
gac acg att atg gct gtg aag aag aat ata gaa gag ata caa ggg aaa 213  
Asp Thr Ile Met Ala Val Lys Lys Asn Ile Glu Glu Ile Gln Gly Lys  
25 30 35  
  
gac agc tat cca tgg ggc caa caa ctg ctg att ttc aat gga aag gtc 261  
Asp Ser Tyr Pro Trp Gly Gln Gln Leu Leu Ile Phe Asn Gly Lys Val  
40 45 50  
  
ttg aaa gat gaa agt aca ttg gaa gag aat aaa gtc aat gag gat ggg 309  
Leu Lys Asp Glu Ser Thr Leu Glu Glu Asn Lys Val Asn Glu Asp Gly  
55 60 65  
  
ttt cta gtt gtc atg ctt agt aag ggt aaa aca tct ggt tca act gga 357  
Phe Leu Val Val Met Leu Ser Lys Gly Lys Thr Ser Gly Ser Thr Gly  
70 75 80  
  
act tca tct tcc cag cac tca aac act cct gca aca agg cag gca cct 405  
Thr Ser Ser Ser Gln His Ser Asn Thr Pro Ala Thr Arg Gln Ala Pro  
85 90 95 100  
  
cct cta gag gcc cca caa caa gct cct caa ccc ccg gtg gca cca att 453

Pro Leu Glu Ala	Pro Gln Gln Ala	Pro Gln Pro	Pro Val Ala	Pro Ile	
105		110		115	
aca act tct cag cct gaa gga ctt cct gca cag gca cct aac aca cat					501
Thr Thr Ser Gln	Pro Glu Gly Leu	Pro Ala Gln Ala	Pro Asn Thr His		
120		125	130		
gac aat gcg gca tca aat ctt ctg tct gga agg aat gtt gac aca ata					549
Asp Asn Ala Ala	Ser Asn Leu Leu	Ser Gly Arg Asn	Val Asp Thr Ile		
135		140	145		
att aac cag cta atg gag atg ggt ggg ggc agt tgg gac aaa gat aaa					597
Ile Asn Gln Leu	Met Glu Met Gly Gly	Ser Trp Asp Lys Asp Lys			
150	155	160			
gtc caa agg gct ctc cgt gcc gct tac aac aac ccc gaa cgt gct gtt					645
Val Gln Arg Ala	Leu Arg Ala Tyr Asn	Asn Pro Glu Arg Ala Val			
165	170	175	180		
gaa tac ctc tac tct ggt att cca gta aca gct gaa att gct gtt cca					693
Glu Tyr Leu Tyr	Ser Gly Ile Pro Val Thr	Ala Glu Ile Ala Val Pro			
185	190	195			
att ggt ggt caa ggg gca aac aca act gat cga gct cct act ggg gaa					741
Ile Gly Gly Gln	Gly Ala Asn Thr Thr Asp Arg Ala	Pro Thr Gly Glu			
200	205	210			
gct ggt ctc tct ggg att cca aac acc gct cca cta gat ctt ttc ccg					789
Ala Gly Leu Ser	Gly Ile Pro Asn Thr Ala	Pro Leu Asp Leu Phe Pro			
215	220	225			
cag ggg gct tcc aat gct gga ggt ggt gct ggt gga cca ctt gat					837
Gln Gly Ala Ser	Asn Ala Gly Gly Gly Ala Gly Gly	Pro Leu Asp			
230	235	240			
ttt ctt aga aac aat cca cag ttt caa gca gtt agg gaa atg gtc cat					885
Phe Leu Arg Asn	Asn Pro Gln Phe Gln Ala Val Arg Glu Met Val His				
245	250	255	260		
aca aat cca caa att ttg cag cct atg ctc gtt gag ttg agc aag cag					933
Thr Asn Pro Gln	Ile Leu Gln Pro Met Leu Val Glu Leu Ser Lys Gln				
265	270	275			
aat cct caa att cta agg ttg att gag gag aat cat gat gag ttt ctt					981
Asn Pro Gln Ile	Leu Arg Leu Ile Glu Glu Asn His Asp Glu Phe Leu				
280	285	290			
cag tta cta aat gag ccc ttt gaa ggc gga gag ggg gat ttc tta gac					1029
Gln Leu Leu Asn	Glu Pro Phe Glu Gly Gly Glu Gly Asp Phe Leu Asp				
295	300	305			
caa cct gag gag gat gaa atg cct cat gcc att agt gtt aca cca gag					1077
Gln Pro Glu Glu	Asp Glu Met Pro His Ala Ile Ser Val Thr Pro Glu				
310	315	320			
gag cag gag gcc att gga cgg ctt gag tcc atg ggg ttc gac aga gca					1125
Glu Gln Glu Ala	Ile Gly Arg Leu Glu Ser Met Gly Phe Asp Arg Ala				
325	330	335	340		
cgc gtt att gaa gca ttc tta gcc tgc gat agg aac gag gag cta gca					1173
Arg Val Ile Glu	Ala Phe Leu Ala Cys Asp Arg Asn Glu Glu Leu Ala				
345	350	355			

gca aac tat ctc ctt gag cat gct ggt gag gaa gat taagcgggag 1219  
Ala Asn Tyr Leu Leu Glu His Ala Gly Glu Glu Asp  
360 365

tagttttcat acgatttttt ttagtaccca gtgacgaaga gttgatattg agctgacgat 1279  
catttgaatt gatttcgttg tgcaagactt gtattacata aacattttaa tacatgtagc 1339  
tgaacatttc agtagaaatg ctacggttgt ggtctcccat cgttgacttt catttagcgtg 1399  
gtggttaaca tcggttctgc tcctgtcctg tattaacaca agcttggctt gggagggaagc 1459  
acaaggagct attgccacct agcaaaaggga taaaaggagg gatgacgaat tggcgatgtg 1519  
tttgcgacac gctgccctca agtgtggatg atgagtgcag ataggttgat gactgtgcca 1579  
aggcgtgtcaa gtgtgttaaac gaacgctgcc ttcgtagtct tgacaaactgc gacagttctg 1639  
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aaa 1702

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<212> PRT  
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Ile Gln Gly Lys Asp Ser Tyr Pro Trp Gly Gln Gln Leu Ile Phe  
35 40 45  
Asn Gly Lys Val Leu Lys Asp Glu Ser Thr Leu Glu Glu Asn Lys Val  
50 55 60  
Asn Glu Asp Gly Phe Leu Val Val Met Leu Ser Lys Gly Lys Thr Ser  
65 70 75 80  
Gly Ser Thr Gly Thr Ser Ser Ser Gln His Ser Asn Thr Pro Ala Thr  
85 90 95  
Arg Gln Ala Pro Pro Leu Glu Ala Pro Gln Gln Ala Pro Gln Pro Pro  
100 105 110  
Val Ala Pro Ile Thr Thr Ser Gln Pro Glu Gly Leu Pro Ala Gln Ala  
115 120 125  
Pro Asn Thr His Asp Asn Ala Ala Ser Asn Leu Leu Ser Gly Arg Asn  
130 135 140  
Val Asp Thr Ile Ile Asn Gln Leu Met Glu Met Gly Gly Gly Ser Trp  
145 150 155 160  
Asp Lys Asp Lys Val Gln Arg Ala Leu Arg Ala Ala Tyr Asn Asn Pro  
165 170 175  
Glu Arg Ala Val Glu Tyr Leu Tyr Ser Gly Ile Pro Val Thr Ala Glu  
180 185 190  
Ile Ala Val Pro Ile Gly Gly Gln Gly Ala Asn Thr Thr Asp Arg Ala  
195 200 205  
Pro Thr Gly Glu Ala Gly Leu Ser Gly Ile Pro Asn Thr Ala Pro Leu  
210 215 220  
Asp Leu Phe Pro Gln Gly Ala Ser Asn Ala Gly Gly Gly Ala Gly Gly  
225 230 235 240  
Gly Pro Leu Asp Phe Leu Arg Asn Asn Pro Gln Phe Gln Ala Val Arg  
245 250 255  
Glu Met Val His Thr Asn Pro Gln Ile Leu Gln Pro Met Leu Val Glu  
260 265 270  
Leu Ser Lys Gln Asn Pro Gln Ile Leu Arg Leu Ile Glu Glu Asn His  
275 280 285  
Asp Glu Phe Leu Gln Leu Leu Asn Glu Pro Phe Glu Gly Gly Glu Gly  
290 295 300  
Asp Phe Leu Asp Gln Pro Glu Glu Asp Glu Met Pro His Ala Ile Ser

305		310		315		320
Val Thr Pro	Glu Glu Gln Glu Ala Ile Gly Arg Leu Glu Ser Met Gly					
	325		330		335	
Phe Asp Arg Ala Arg Val Ile Glu Ala Phe Leu Ala Cys Asp Arg Asn						
	340		345		350	
Glu Glu Leu Ala Ala Asn Tyr Leu Leu Glu His Ala Gly Glu Glu Asp						
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<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide based upon an adaptor used for cDNA library construction and poly(dT) to remove clones which have a poly(A) tail but no cDNA insert.

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36